



85

A1

1977-1978
 1979-1980
 1981-1982
 1983-1984
 1985-1986
 1987-1988
 1989-1990
 1991-1992
 1993-1994
 1995-1996
 1997-1998
 1999-2000
 2001-2002
 2003-2004
 2005-2006
 2007-2008
 2009-2010
 2011-2012
 2013-2014
 2015-2016
 2017-2018
 2019-2020
 2021-2022
 2023-2024
 2025-2026
 2027-2028
 2029-2030
 2031-2032
 2033-2034
 2035-2036
 2037-2038
 2039-2040
 2041-2042
 2043-2044
 2045-2046
 2047-2048
 2049-2050
 2051-2052
 2053-2054
 2055-2056
 2057-2058
 2059-2060
 2061-2062
 2063-2064
 2065-2066
 2067-2068
 2069-2070
 2071-2072
 2073-2074
 2075-2076
 2077-2078
 2079-2080
 2081-2082
 2083-2084
 2085-2086
 2087-2088
 2089-2090
 2091-2092
 2093-2094
 2095-2096
 2097-2098
 2099-2100
 2101-2102
 2103-2104
 2105-2106
 2107-2108
 2109-2110
 2111-2112
 2113-2114
 2115-2116
 2117-2118
 2119-2120
 2121-2122
 2123-2124
 2125-2126
 2127-2128
 2129-2130
 2131-2132
 2133-2134
 2135-2136
 2137-2138
 2139-2140
 2141-2142
 2143-2144
 2145-2146
 2147-2148
 2149-2150
 2151-2152
 2153-2154
 2155-2156
 2157-2158
 2159-2160
 2161-2162
 2163-2164
 2165-2166
 2167-2168
 2169-2170
 2171-2172
 2173-2174
 2175-2176
 2177-2178
 2179-2180
 2181-2182
 2183-2184
 2185-2186
 2187-2188
 2189-2190
 2191-2192
 2193-2194
 2195-2196
 2197-2198
 2199-2200
 2201-2202
 2203-2204
 2205-2206
 2207-2208
 2209-2210
 2211-2212
 2213-2214
 2215-2216
 2217-2218
 2219-2220
 2221-2222
 2223-2224
 2225-2226
 2227-2228
 2229-2230
 2231-2232
 2233-2234
 2235-2236
 2237-2238
 2239-2240
 2241-2242
 2243-2244
 2245-2246
 2247-2248
 2249-2250
 2251-2252
 2253-2254
 2255-2256
 2257-2258
 2259-2260
 2261-2262
 2263-2264
 2265-2266
 2267-2268
 2269-2270
 2271-2272
 2273-2274
 2275-2276
 2277-2278
 2279-2280
 2281-2282
 2283-2284
 2285-2286
 2287-2288
 2289-2290
 2291-2292
 2293-2294
 2295-2296
 2297-2298
 2299-2300
 2301-2302
 2303-2304
 2305-2306
 2307-2308
 2309-2310
 2311-2312
 2313-2314
 2315-2316
 2317-2318
 2319-2320
 2321-2322
 2323-2324
 2325-2326
 2327-2328
 2329-2330
 2331-2332
 2333-2334
 2335-2336
 2337-2338
 2339-2340
 2341-2342
 2343-2344
 2345-2346
 2347-2348
 2349-2350
 2351-2352
 2353-2354
 2355-2356
 2357-2358
 2359-2360
 2361-2362
 2363-2364
 2365-2366
 2367-2368
 2369-2370
 2371-2372
 2373-2374
 2375-2376
 2377-2378
 2379-2380
 2381-2382
 2383-2384
 2385-2386
 2387-2388
 2389-2390
 2391-2392
 2393-2394
 2395-2396
 2397-2398
 2399-2400
 2401-2402
 2403-2404
 2405-2406
 2407-2408
 2409-2410
 2411-2412
 2413-2414
 2415-2416
 2417-2418
 2419-2420
 2421-2422
 2423-2424
 2425-2426
 2427-2428
 2429-2430
 2431-2432
 2433-2434
 2435-2436
 2437-2438
 2439-2440
 2441-2442
 2443-2444
 2445-2446
 2447-2448
 2449-2450
 2451-2452
 2453-2454
 2455-2456
 2457-2458
 2459-2460
 2461-2462
 2463-2464
 2465-2466
 2467-2468
 2469-2470
 2471-2472
 2473-2474
 2475-2476
 2477-2478
 2479-2480
 2481-2482
 2483-2484
 2485-2486
 2487-2488
 2489-2490
 2491-2492
 2493-2494
 2495-2496
 2497-2498
 2499-2500
 2501-2502
 2503-2504
 2505-2506
 2507-2508
 2509-2510
 2511-2512
 2513-2514
 2515-2516
 2517-2518
 2519-2520
 2521-2522
 2523-2524
 2525-2526
 2527-2528
 2529-2530
 2531-2532
 2533-2534
 2535-2536
 2537-2538
 2539-2540
 2541-2542
 2543-2544
 2545-2546
 2547-2548
 2549-2550
 2551-2552
 2553-2554
 2555-2556
 2557-2558
 2559-2560
 256

Ala Ala Glu Arg Gln Arg Glu Gln Tyr Trp Glu Glu Lys Glu Gln Thr	
315 320 325	
ctg ctg cag ttc cag aag agt aag atg gcc tgc caa ctc tac agg gag	1241
Leu Leu Gln Phe Gln Lys Ser Lys Met Ala Cys Gln Leu Tyr Arg Glu	
330 335 340 345	
aag gtg aat gcg ctg cag gcc cag gtg tgc gag ctg cag aag gag cga	1289
Lys Val Asn Ala Leu Gln Ala Gln Val Cys Glu Leu Gln Lys Glu Arg	
350 355 360	
gac cag gcg tac tcc gcg agg gac agt gct cag agg gag att tcc cag	1337
Asp Gln Ala Tyr Ser Ala Arg Asp Ser Ala Gln Arg Glu Ile Ser Gln	
365 370 375	
agc ctg gtg gag aag gac tcc ctc cgc agg cag gtg ttc gag ctg acg	1385
Ser Leu Val Glu Lys Asp Ser Leu Arg Arg Gln Val Phe Glu Leu Thr	
380 385 390	
gac cag gtc tgc gag ctg cgc aca cag ctt cgc cag ctg cag gca gag	1433
Asp Gln Val Cys Glu Leu Arg Thr Gln Leu Arg Gln Leu Gln Ala Glu	
395 400 405	
cct ccg ggt gtg ctc aag cag gaa gcc agg acc agg gag ccc tgt cca	1481
Pro Pro Gly Val Leu Lys Gln Glu Ala Arg Thr Arg Glu Pro Cys Pro	
410 415 420 425	
cgg gag aag cag cgg ctg gtg cgg atg cat gcc atc tgc ccc aga gac	1529
Arg Glu Lys Gln Arg Leu Val Arg Met His Ala Ile Cys Pro Arg Asp	
430 435 440	
gac agc gac tgc agc ctc gtc agc tcc aca gag tct cag ctc ttg tcg	1577
Asp Ser Asp Cys Ser Leu Val Ser Ser Thr Glu Ser Gln Leu Leu Ser	
445 450 455	
gac ctg agt gcc acg tcc agc cgc gag ctg gtg gac agc ttc cgc tcc	1625
Asp Leu Ser Ala Thr Ser Ser Arg Glu Leu Val Asp Ser Phe Arg Ser	
460 465 470	
agc agc ccc gcg ccc ccc agc cag cag tcc ctg tac aag cgg gtg gcc	1673
Ser Ser Pro Ala Pro Pro Ser Gln Gln Ser Leu Tyr Lys Arg Val Ala	
475 480 485	
gag gac ttc ggg gaa gaa ccc tgg tct ttc agc agc tgc ctg gag atc	1721
Glu Asp Phe Gly Glu Glu Pro Trp Ser Phe Ser Ser Cys Leu Glu Ile	
490 495 500 505	
ccg gag gga gac ccg gga gcc ctg ccg gga gct aag gca ggc gac cca	1769
Pro Glu Gly Asp Pro Gly Ala Leu Pro Gly Ala Lys Ala Gly Asp Pro	
510 515 520	
cac ctg gat tat gag ctc cta gac acg gca gac ctt ccg cag ctg gaa	1817
His Leu Asp Tyr Glu Leu Leu Asp Thr Ala Asp Leu Pro Gln Leu Glu	
525 530 535	
agc agc ctg cag cca gtc tcc cct gga agg ctt gat gtc tcg gag agc	1865
Ser Ser Leu Gln Pro Val Ser Pro Gly Arg Leu Asp Val Ser Glu Ser	

A1

F00369-9460

540	545	550	
ggc gtc ctc atg cgg cgg agg cca gcc cgc agg atc ctg agc cag gtc Gly Val Leu Met Arg Arg Arg Pro Ala Arg Arg Ile Leu Ser Gln Val 555 560 565			1913
acc atg ctg gcg ttc cag ggg gat gca ttg ctg gag cag atc agc gtc Thr Met Leu Ala Phe Gln Gly Asp Ala Leu Leu Glu Gln Ile Ser Val 570 575 580 585			1961
atc ggc ggg aac ctc acg ggc atc ttc atc cac cgc gtc acc ccg ggc Ile Gly Gly Asn Leu Thr Gly Ile Phe Ile His Arg Val Thr Pro Gly 590 595 600			2009
tcg gcg gcg gac cag atg gcc ttg cgc ccg ggc acc cag att gtg atg Ser Ala Ala Asp Gln Met Ala Leu Arg Pro Gly Thr Gln Ile Val Met 605 610 615			2057
gtt gat tac gaa gcc tca gag ccc ttg ttc aag gca gtc ctg gag gac Val Asp Tyr Glu Ala Ser Glu Pro Leu Phe Lys Ala Val Leu Glu Asp 620 625 630			2105
acg acc ctg gag gag gcc gtg ggg ctt ctc agg agg gtg gac ggc ttc Thr Thr Leu Glu Glu Ala Val Gly Leu Leu Arg Arg Val Asp Gly Phe 635 640 645			2153
tgc tgc ctg tct gtg aag gtc aac acg gac ggt tat aag agg cta ctc Cys Cys Leu Ser Val Lys Val Asn Thr Asp Gly Tyr Lys Arg Leu Leu 650 655 660 665			2201
cag gac ctg gag gcc aaa gtg gcg acc tcg ggg gac tca ttc tac atc Gln Asp Leu Glu Ala Lys Val Ala Thr Ser Gly Asp Ser Phe Tyr Ile 670 675 680			2249
cgg gtc aac ctg gcc atg gag ggc agg gcc aaa ggg gag ctg cag gtg Arg Val Asn Leu Ala Met Glu Gly Arg Ala Lys Gly Glu Leu Gln Val 685 690 695			2297
cat tgc aac gag gtc ctg cac gtc acc gac acc atg ttc cag ggc tgc His Cys Asn Glu Val Leu His Val Thr Asp Thr Met Phe Gln Gly Cys 700 705 710			2345
ggc tgc tgg cat gcc cac cgc gtg aac tct tac acc atg aag gat act Gly Cys Trp His Ala His Arg Val Asn Ser Tyr Thr Met Lys Asp Thr 715 720 725			2393
gcc gcg cac ggc acc atc ccc aac tac tcc agg gct cag cag cag ctc Ala Ala His Gly Thr Ile Pro Asn Tyr Ser Arg Ala Gln Gln Gln Leu 730 735 740 745			2441
ata gcc ctc atc cag gac atg act cag cag tgc acc gtg acc cgc aag Ile Ala Leu Ile Gln Asp Met Thr Gln Gln Cys Thr Val Thr Arg Lys 750 755 760			2489
cca tct tct ggg gga cca cag aag ctg gtc cgc atc gtc agt atg gac Pro Ser Ser Gly Gly Pro Gln Lys Leu Val Arg Ile Val Ser Met Asp 765 770 775			2537

A1

0075745-053004

aaa gcc aag gcc agc cct ctg cgt ttg tcc ttt gac agg ggc cag ttg 2585
 Lys Ala Lys Ala Ser Pro Leu Arg Leu Ser Phe Asp Arg Gly Gln Leu
 780 785 790

gac ccc agc agg atg gag ggc tcc agc acg tgc ttc tgg gcc gag agc 2633
 Asp Pro Ser Arg Met Glu Gly Ser Ser Thr Cys Phe Trp Ala Glu Ser
 795 800 805

tgc ctc acc ctg gtg ccc tat acc ctg gtg tgg ccc cat cga ccc gcc 2681
 Cys Leu Thr Leu Val Pro Tyr Thr Leu Val Trp Pro His Arg Pro Ala
 810 815 820 825

cgg ccc cgg cct gtg ctc ctc gtg ccc agg gcg gtt ggg aag atc ctg 2729
 Arg Pro Arg Pro Val Leu Leu Val Pro Arg Ala Val Gly Lys Ile Leu
 830 835 840

agc gag aaa ctg tgc ctc ctc caa ggg ttt aag aag tgc ctg gca gag 2777
 Ser Glu Lys Leu Cys Leu Leu Gln Gly Phe Lys Lys Cys Leu Ala Glu
 845 850 855

tac ttg agc cag gag gag tat gag gcc tgg agc cag aga ggg gac atc 2825
 Tyr Leu Ser Gln Glu Glu Tyr Glu Ala Trp Ser Gln Arg Gly Asp Ile
 860 865 870

atc cag gag gga gag gtg tcc ggg ggc cgc tgc tgg gtg acc cgc cat 2873
 Ile Gln Glu Gly Glu Val Ser Gly Gly Arg Cys Trp Val Thr Arg His
 875 880 885

gct gtg gag tcc ctc atg gaa aag aac acc cat gcc ctc ctg gac gtc 2921
 Ala Val Glu Ser Leu Met Glu Lys Asn Thr His Ala Leu Leu Asp Val
 890 895 900 905

cag ctg gac agt gtc tgc acc ctg cac agg atg gac atc ttc ccc atc 2969
 Gln Leu Asp Ser Val Cys Thr Leu His Arg Met Asp Ile Phe Pro Ile
 910 915 920

gtc atc cac gtc tct gtc aac gag aag atg gca aag aag ctc aag aag 3017
 Val Ile His Val Ser Val Asn Glu Lys Met Ala Lys Lys Leu Lys Lys
 925 930 935

ggc cta cag cgg ttg ggc acc tca gag gag cag ctc ctg gag gct gcg 3065
 Gly Leu Gln Arg Leu Gly Thr Ser Glu Glu Gln Leu Leu Glu Ala Ala
 940 945 950

agg cag gag gag gga gac ctg gac cgg gcg ccc tgt cta tac agc agc 3113
 Arg Gln Glu Glu Gly Asp Leu Asp Arg Ala Pro Cys Leu Tyr Ser Ser
 955 960 965

ctg gct cct gac ggc tgg agc gac ctg gac ggc ctg ctc agc tgt gtc 3161
 Leu Ala Pro Asp Gly Trp Ser Asp Leu Asp Gly Leu Leu Ser Cys Val
 970 975 980 985

cgc cag gcc atc gcc gac gag cag aag aag gtg gtg tgg acg gag cag 3209
 Arg Gln Ala Ile Ala Asp Glu Gln Lys Lys Val Val Trp Thr Glu Gln
 990 995 1000

00767415-060001

A

agc ccc cga tgatgcaccg tgcccccttc cgggactgtg ggggcttctg
Ser Pro Arg

3258

tgtgcctggt aatgcagtc tggttcctcag cccaggccct cttggcacag ctgtgggctc 3318
cttggcacat gaggccggt ctccccactg gctggggtct aaccttgaac cctcaccacg 3378
tgcaggtcac acacagtga gccacttgta actgcacact tttctgtgga aacatcttca 3438
ccctttacca ggcttggcat ggtctgaact ggaaacctg agaatgtttc tgcagtagga 3498
caggagggac atcttcccat gccttcccta gaaccggagg ccccggaact ctctggaaaa 3558
ccgctgtct gcaggcccga ttcaaatacta tgggggctgc acttcccttt tacattttga 3618
tgtgtcaaag gcttttggag tgaccaaag cacagaggca gcgggtgggg cgctgggtg 3678
gtccccaagg tcgctgccac ccttgcccg ggagaggca taagcccaca tatgctgtga 3738
cgctggccac cttttctcag cttctgaggc tgcgatgcct caggaactcc agtttacaga 3798
gaccagtgtg tttacttgta aataaagcct ctgggtgggt gagacggtac tttcagtggg 3858
tctgtgcccc gtggccctg tgccgtgttcg gtgggggtgt cccagagaag cctggcacca 3918
gtacccccgt caa 3931

<210> 2

<211> 1004

<212> PRT

<213> Homo sapiens

<400> 2

Met Gly Glu Leu Cys Arg Arg Asp Ser Ala Leu Thr Ala Leu Asp Glu
1 5 10 15
Glu Thr Leu Trp Glu Met Met Glu Ser His Arg His Arg Ile Val Arg
20 25 30
Cys Ile Cys Pro Ser Arg Leu Thr Pro Tyr Leu Arg Gln Ala Lys Val
35 40 45
Leu Cys Gln Leu Asp Glu Glu Val Leu His Ser Pro Arg Leu Thr
50 55 60
Asn Ser Ala Met Arg Ala Gly His Leu Leu Asp Leu Leu Lys Thr Arg
65 70 75 80
Gly Lys Asn Gly Ala Ile Ala Phe Leu Glu Ser Leu Lys Phe His Asn
85 90 95
Pro Asp Val Tyr Thr Leu Val Thr Gly Leu Gln Pro Asp Val Asp Phe
100 105 110
Ser Asn Phe Ser Gly Leu Met Glu Thr Ser Lys Leu Thr Glu Cys Leu
115 120 125
Ala Gly Ala Ile Gly Ser Leu Gln Glu Glu Leu Asn Gln Glu Lys Gly
130 135 140
Gln Lys Glu Val Leu Leu Arg Arg Cys Gln Gln Leu Gln Glu His Leu
145 150 155 160
Gly Leu Ala Glu Thr Arg Ala Glu Gly Leu His Gln Leu Glu Ala Asp
165 170 175
His Ser Arg Met Lys Arg Glu Val Ser Ala His Phe His Glu Val Leu
180 185 190
Arg Leu Lys Asp Glu Met Leu Ser Leu Ser Leu His Tyr Ser Asn Ala
195 200 205
Leu Gln Glu Lys Glu Leu Ala Ala Ser Arg Cys Arg Ser Leu Gln Glu
210 215 220
Glu Leu Tyr Leu Leu Lys Gln Glu Leu Gln Arg Ala Asn Met Val Ser
225 230 235 240
Ser Cys Glu Leu Glu Leu Gln Glu Gln Ser Leu Arg Thr Ala Ser Asp
245 250 255
Gln Glu Ser Gly Asp Glu Glu Leu Asn Arg Leu Lys Glu Glu Asn Glu
260 265 270

A1

F00293.5.3460

Lys Leu Arg Ser Leu Thr Phe Ser Leu Ala Glu Lys Asp Ile Leu Glu
 275 280 285
 Gln Ser Leu Asp Glu Ala Arg Gly Ser Arg Gln Glu Leu Val Glu Arg
 290 295 300
 Ile His Ser Leu Arg Glu Arg Ala Val Ala Ala Glu Arg Gln Arg Glu
 305 310 315 320
 Gln Tyr Trp Glu Glu Lys Glu Gln Thr Leu Leu Gln Phe Gln Lys Ser
 325 330 335
 Lys Met Ala Cys Gln Leu Tyr Arg Glu Lys Val Asn Ala Leu Gln Ala
 340 345 350
 Gln Val Cys Glu Leu Gln Lys Glu Arg Asp Gln Ala Tyr Ser Ala Arg
 355 360 365
 Asp Ser Ala Gln Arg Glu Ile Ser Gln Ser Leu Val Glu Lys Asp Ser
 370 375 380
 Leu Arg Arg Gln Val Phe Glu Leu Thr Asp Gln Val Cys Glu Leu Arg
 385 390 395 400
 Thr Gln Leu Arg Gln Leu Gln Ala Glu Pro Pro Gly Val Leu Lys Gln
 405 410 415
 Glu Ala Arg Thr Arg Glu Pro Cys Pro Arg Glu Lys Gln Arg Leu Val
 420 425 430
 Arg Met His Ala Ile Cys Pro Arg Asp Asp Ser Asp Cys Ser Leu Val
 435 440 445
 Ser Ser Thr Glu Ser Gln Leu Leu Ser Asp Leu Ser Ala Thr Ser Ser
 450 455 460
 Arg Glu Leu Val Asp Ser Phe Arg Ser Ser Ser Pro Ala Pro Pro Ser
 465 470 475 480
 Gln Gln Ser Leu Tyr Lys Arg Val Ala Glu Asp Phe Gly Glu Glu Pro
 485 490 495
 Trp Ser Phe Ser Ser Cys Leu Glu Ile Pro Glu Gly Asp Pro Gly Ala
 500 505 510
 Leu Pro Gly Ala Lys Ala Gly Asp Pro His Leu Asp Tyr Glu Leu Leu
 515 520 525
 Asp Thr Ala Asp Leu Pro Gln Leu Glu Ser Ser Leu Gln Pro Val Ser
 530 535 540
 Pro Gly Arg Leu Asp Val Ser Glu Ser Gly Val Leu Met Arg Arg Arg
 545 550 555 560
 Pro Ala Arg Arg Ile Leu Ser Gln Val Thr Met Leu Ala Phe Gln Gly
 565 570 575
 Asp Ala Leu Leu Glu Gln Ile Ser Val Ile Gly Gly Asn Leu Thr Gly
 580 585 590
 Ile Phe Ile His Arg Val Thr Pro Gly Ser Ala Ala Asp Gln Met Ala
 595 600 605
 Leu Arg Pro Gly Thr Gln Ile Val Met Val Asp Tyr Glu Ala Ser Glu
 610 615 620
 Pro Leu Phe Lys Ala Val Leu Glu Asp Thr Thr Leu Glu Glu Ala Val
 625 630 635 640
 Gly Leu Leu Arg Arg Val Asp Gly Phe Cys Cys Leu Ser Val Lys Val
 645 650 655
 Asn Thr Asp Gly Tyr Lys Arg Leu Leu Gln Asp Leu Glu Ala Lys Val
 660 665 670
 Ala Thr Ser Gly Asp Ser Phe Tyr Ile Arg Val Asn Leu Ala Met Glu
 675 680 685
 Gly Arg Ala Lys Gly Glu Leu Gln Val His Cys Asn Glu Val Leu His
 690 695 700
 Val Thr Asp Thr Met Phe Gln Gly Cys Gly Cys Trp His Ala His Arg
 705 710 715 720
 Val Asn Ser Tyr Thr Met Lys Asp Thr Ala Ala His Gly Thr Ile Pro

A1

00767215-052004

[illegible]

<400> 3

atgggggaac	tgtgccgcag	ggactccgca	ctcacggcac	tggacgagga	gacactgtgg	60
gagatgatgg	agagccaccg	ccacaggatc	gtacgctgca	tctgccccag	ccgcctcacc	120
ccctacctgc	gccaggccaa	ggtgctgtgc	cagctggacg	aggaggaggt	gctgcacagc	180
ccccggctca	ccaacagcgc	catgcgggcc	gggcacttgc	tggatttgct	gaagactcga	240
gggaagaacg	gggccatcgc	cttcctggag	agcctgaagt	tccacaaccc	tgacgtctac	300
accctggtca	ccgggctgca	gcctgatgtt	gacttcagta	actttagcgg	tctcatggag	360
acatccaagc	tgaccgagtg	cctggctggg	gccatcggca	gcctgcagga	ggagctgaac	420
caggaaaagg	ggcagaagga	ggtgctgctg	cggcggtgcc	agcagctgca	ggagcacctg	480
ggcttggccg	agaccctgtc	cgagggcctg	caccagctgg	aggctgacca	cagccgcatg	540
aagcgtgagg	ttagcgcaca	cttccatgag	gtgctgaggc	tgaaggacga	gatgctcagc	600
ctctcgctgc	actatagcaa	tgcctgcgac	gagaaggagc	tggccgcctc	acgctgccgc	660
agcctgcagg	aggagctgta	tctactgaag	caggagctgc	agcgagccaa	catggtttcc	720
tctctgtagc	tgaatttgca	agagcagtc	ctgaggacag	ccagcgacca	ggagttccgg	780
gatgaggagc	tgaaccgcct	gaaggaggag	aatgagaaac	tcgcctcgct	gactttcagc	840
ctggcgggaga	aggacattct	ggagcagagc	ctggacgagg	cgcgggggag	ccgacaggag	900

ctggtggagc gcatccactc gctgcgggag cgggccgtgg ctgccgagag gcagcgagag 960
cagtactggg aagagaagga acagaccctg ctgcagttcc agaagagtaa gatggcctgc 1020
caactctaca gggagaaggt gaatgcgctg caggcccagg tgtgcgagct gcagaaggag 1080
cgagaccagg cgtactccgc gagggacagt gctcagaggg agatttccca gaggcctggtg 1140
gagaaggact ccctccgcag gcagggtgttc gagctgacgg accaggctctg cgagctgcgc 1200
acacagcttc gccagctgca ggcagagcct ccgggtgtgc tcaagcagga agccaggacc 1260
agggagccct gtccacggga gaagcagcgg ctggtgcgga tgcattgccat ctgccccaga 1320
gacgacagcg actgcagcct cgtcagctcc acagagtctc agctcttgct ggacctgagt 1380
gccacgtcca gccgcgagct ggtggacagc ttccgctcca gcagccccgc gccccccagc 1440
cagcagtcct tgtacaagcg ggtggccgag gacttcgggg aagaaccctg gtctttcagc 1500
agctgcctgg agatcccga gggagaccgg ggagccctgc cgggagctaa ggcaggcgac 1560
ccacacctgg attatgagct cctagacacg gcagaccttc cgcagctgga aagcagcctg 1620
cagccagtct cccctggaag gcttgatgtc tcggagagcg gcgtcctcat gcggcggagg 1680
ccagcccga ggatcctgag ccaggtcacc atgctggcgt tccagggga tgcattgctg 1740
gagcagatca gcgtcatcgg cgggaacctc acgggcatct tcatccaccg ggtcaccccg 1800
ggctcggcgg cggaccagat ggcttgcgc ccgggcaccc agattgtgat ggttgattac 1860
gaagcctcag agcccttgtt caaggcagtc ctggaggaca cagccctgga ggaggccgtg 1920
gggcttctca ggagggtgga cggcttctgc tgctgtctg tgaaggtaa cacggacggt 1980
tataagaggc tactccagga cctggaggcc aaagtggcga cctcggggga ctcatctac 2040
atccgggtca acctggccat ggagggcagg gccaaagggg agctgcaggt gcattgcaac 2100
gaggtcctgc acgtcaccga caccatgttc cagggtcgc gctgctggca tgccaccgc 2160
gtgaactctt acaccatgaa ggatactgcc gcgcacggca ccatcccaa ctactccagg 2220
gctcagcagc agctcatagc cctcatccag gacatgactc agcagtgcac cgtgaccgc 2280
aagccatctt ctgggggacc acagaagctg gtccgcacg tcaagtatgga caaagccaag 2340
gccagccctc tgcgtttgtc ctttgacagg ggccagttgg accccagcag gatggagggc 2400
tccagcacgt gcttctgggc cgagagctgc ctacccctgg tgccctatac cctggtgtgg 2460
ccccatcgac ccgcccggcc ccggcctgtg ctctcgtgc ccagggcggg tgggaagatc 2520
ctgagcgaga aactgtgcct cctccaaggg ttttaagaag gcctggcaga gtacttgagc 2580
caggaggagt atgaggcctg gagccagaga ggggacatca tccaggaggg agaggtgtcc 2640
gggggcccgt gctgggtgac ccgccatgct gtggagtccc tcatggaaaa gaacacccat 2700
ggcctcctgg acgtccagct ggacagtgtc tgcacctgc acaggatgga catcttcccc 2760
atcgtcatcc acgtctctgt caacgagaag atggcaaga agctcaagaa gggcctacag 2820
cggttgggca cctcagagga gcagctcctg gaggtgcga ggcaggagga gggagacctg 2880
gaccgggcgc cctgtctata cagcagcctg gctcctgacg gctggagcga cctggacggc 2940
ctgctcagct gtgtccgcca ggccatcgcc gacgagcaga agaagggtgt gtggacggag 3000
cagagccccc ga 3012

<210> 4
<211> 3417
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(3417)

<400> 4
atg ggg gaa ctg tgc cgc agg gac tcc gca ctc acg gca ctg gac gag 48
Met Gly Glu Leu Cys Arg Arg Asp Ser Ala Leu Thr Ala Leu Asp Glu
1 5 10 15
gag aca ctg tgg gag atg atg gag agc cac cgc cac agg atc gta cgc 96
Glu Thr Leu Trp Glu Met Met Glu Ser His Arg His Arg Ile Val Arg
20 25 30
tgc atc tgc ccc agc cgc ctc acc ccc tac ctg cgc cag gcc aag gtg 144
Cys Ile Cys Pro Ser Arg Leu Thr Pro Tyr Leu Arg Gln Ala Lys Val

35				40				45								
ctg	tgc	cag	ctg	gac	gag	gag	gag	gtg	ctg	cac	agc	ccc	cgg	ctc	acc	192
Leu	Cys	Gln	Leu	Asp	Glu	Glu	Glu	Val	Leu	His	Ser	Pro	Arg	Leu	Thr	
50						55				60						
aac	agc	gcc	atg	cgg	gcc	ggg	cac	ttg	ctg	gat	ttg	ctg	aag	act	cga	240
Asn	Ser	Ala	Met	Arg	Ala	Gly	His	Leu	Leu	Asp	Leu	Leu	Lys	Thr	Arg	
65						70				75						80
ggg	aag	aac	ggg	gcc	atc	gcc	ttc	ctg	gag	agc	ctg	aag	ttc	cac	aac	288
Gly	Lys	Asn	Gly	Ala	Ile	Ala	Phe	Leu	Glu	Ser	Leu	Lys	Phe	His	Asn	
				85				90						95		
cct	gac	gtc	tac	acc	ctg	gtc	acc	ggg	ctg	cag	cct	gat	gtt	gac	ttc	336
Pro	Asp	Val	Tyr	Thr	Leu	Val	Thr	Gly	Leu	Gln	Pro	Asp	Val	Asp	Phe	
		100						105				110				
agt	aac	ttt	agc	ggg	gag	agc	tcc	gac	ttt	gac	ggg	ttg	gca	ggc	act	384
Ser	Asn	Phe	Ser	Gly	Glu	Ser	Ser	Asp	Phe	Asp	Gly	Leu	Ala	Gly	Thr	
		115				120						125				
tct	agg	aac	ctc	agg	ctc	ctg	gta	acc	cca	ggg	ctc	atg	gag	aca	tcc	432
Ser	Arg	Asn	Leu	Arg	Leu	Leu	Val	Thr	Pro	Gly	Leu	Met	Glu	Thr	Ser	
130						135				140						
aag	ctg	acc	gag	tgc	ctg	gct	ggg	gcc	atc	ggc	agc	ctg	cag	gag	gag	480
Lys	Leu	Thr	Glu	Cys	Leu	Ala	Gly	Ala	Ile	Gly	Ser	Leu	Gln	Glu	Glu	
145				150						155				160		
ctg	aac	cag	gaa	aag	ggg	cag	aag	gag	gtg	ctg	ctg	cgg	cgg	tgc	cag	528
Leu	Asn	Gln	Glu	Lys	Gly	Gln	Lys	Glu	Val	Leu	Leu	Arg	Arg	Cys	Gln	
				165				170						175		
cag	ctg	cag	gag	cac	ctg	ggc	ctg	gcc	gag	acc	cgt	gcc	gag	ggc	ctg	576
Gln	Leu	Gln	Glu	His	Leu	Gly	Leu	Ala	Glu	Thr	Arg	Ala	Glu	Gly	Leu	
		180				185						190				
cac	cag	ctg	gag	gct	gac	cac	agc	cgc	atg	aag	cgt	gag	gtt	agc	gca	624
His	Gln	Leu	Glu	Ala	Asp	His	Ser	Arg	Met	Lys	Arg	Glu	Val	Ser	Ala	
195						200				205						
cac	ttc	cat	gag	gtg	ctg	agg	ctg	aag	gac	gag	atg	ctc	agc	ctc	tcg	672
His	Phe	His	Glu	Val	Leu	Arg	Leu	Lys	Asp	Glu	Met	Leu	Ser	Leu	Ser	
210						215				220						
ctg	cac	tat	agc	aat	gcg	ctg	cag	gag	aag	gag	ctg	gcc	gcc	tca	cgc	720
Leu	His	Tyr	Ser	Asn	Ala	Leu	Gln	Glu	Lys	Glu	Leu	Ala	Ala	Ser	Arg	
225				230						235				240		
tgc	cgc	agc	ctg	cag	gag	gag	ctg	tat	cta	ctg	aag	cag	gag	ctg	cag	768
Cys	Arg	Ser	Leu	Gln	Glu	Glu										

ctg agg aca gcc agc gac cag gag tcc ggg gat gag gag ctg aac cgc 864
 Leu Arg Thr Ala Ser Asp Gln Glu Ser Gly Asp Glu Glu Leu Asn Arg
 275 280 285

ctg aag gag gag aat gag aaa ctg cgc tcc ctg act ttc agc ctg gcg 912
 Leu Lys Glu Glu Asn Glu Lys Leu Arg Ser Leu Thr Phe Ser Leu Ala
 290 295 300

gag aag gac att ctg gag cag agc ctg gac gag gcg cgg ggg agc cga 960
 Glu Lys Asp Ile Leu Glu Gln Ser Leu Asp Glu Ala Arg Gly Ser Arg
 305 310 315 320

cag gag ctg gtg gag cgc atc cac tcc ctg cgg gag cgg gcc gtg gct 1008
 Gln Glu Leu Val Glu Arg Ile His Ser Leu Arg Glu Arg Ala Val Ala
 325 330 335

gcc gag agg cag cga gag cag gcc aga ccc tca gag ctg ctg agc ttc 1056
 Ala Glu Arg Gln Arg Glu Gln Ala Arg Pro Ser Glu Leu Leu Ser Phe
 340 345 350

acg gtc cat gtg tcc cac tct gtc cag tac tgg gaa gag aag gaa cag 1104
 Thr Val His Val Ser His Ser Val Gln Tyr Trp Glu Glu Lys Glu Gln
 355 360 365

acc ctg ctg cag ttc cag aag agt aag atg gcc tgc caa ctc tac agg 1152
 Thr Leu Leu Gln Phe Gln Lys Ser Lys Met Ala Cys Gln Leu Tyr Arg
 370 375 380

gag aag gtg aat gcg ctg cag gcc cag gtg tgc gag ctg cag aag gag 1200
 Glu Lys Val Asn Ala Leu Gln Ala Gln Val Cys Glu Leu Gln Lys Glu
 385 390 395 400

cga gac cag gcg tac tcc gcg agg gac agt gct cag agg gag att tcc 1248
 Arg Asp Gln Ala Tyr Ser Ala Arg Asp Ser Ala Gln Arg Glu Ile Ser
 405 410 415

cag agc ctg gtg gag aag gac tcc ctc cgc agg cag gtg ttc gag ctg 1296
 Gln Ser Leu Val Glu Lys Asp Ser Leu Arg Arg Gln Val Phe Glu Leu
 420 425 430

acg gac cag gtc tgc gag ctg cgc aca cag ctt cgc cag ctg cag gca 1344
 Thr Asp Gln Val Cys Glu Leu Arg Thr Gln Leu Arg Gln Leu Gln Ala
 435 440 445

gag cct ccg ggt gtg ctc aag cag gaa gcc agg acc agg gag ccc tgt 1392
 Glu Pro Pro Gly Val Leu Lys Gln Glu Ala Arg Thr Arg Glu Pro Cys
 450 455 460

cca cgg gag aag cag cgg ctg gtg cgg atg cat gcc atc tgc ccc aga 1440
 Pro Arg Glu Lys Gln Arg Leu Val Arg Met His Ala Ile Cys Pro Arg
 465 470 475 480

gac gac agc gac tgc agc ctc gtc agc tcc aca gag tct cag ctc ttg 1488
 Asp Asp Ser Asp Cys Ser Leu Val Ser Ser Thr Glu Ser Gln Leu Leu
 485 490 495

A

T00250-51250

tcg gac ctg agt gcc acg tcc agc cgc gag ctg gtg gac agc ttc cgc	1536
Ser Asp Leu Ser Ala Thr Ser Ser Arg Glu Leu Val Asp Ser Phe Arg	
500 505 510	
tcc agc agc ccc gcg ccc ccc agc cag cag tcc ctg tac aag cgg gtg	1584
Ser Ser Ser Pro Ala Pro Pro Ser Gln Gln Ser Leu Tyr Lys Arg Val	
515 520 525	
gcc gag gac ttc ggg gaa gaa ccc tgg tct ttc agc agc tgc ctg gag	1632
Ala Glu Asp Phe Gly Glu Glu Pro Trp Ser Phe Ser Ser Cys Leu Glu	
530 535 540	
atc ccg gag gga gac ccg gga gcc ctg ccg gga gct aag gca ggc gac	1680
Ile Pro Glu Gly Asp Pro Gly Ala Leu Pro Gly Ala Lys Ala Gly Asp	
545 550 555 560	
cca cac ctg gat tat gag ctc cta gac acg gca gac ctt ccg cag ctg	1728
Pro His Leu Asp Tyr Glu Leu Leu Asp Thr Ala Asp Leu Pro Gln Leu	
565 570 575	
gaa agc agc ctg cag cca gtc tcc cct gga agg ctt gat gtc tcg gag	1776
Glu Ser Ser Leu Gln Pro Val Ser Pro Gly Arg Leu Asp Val Ser Glu	
580 585 590	
agt gca caa gcc ggt cgt ctc ccg gcc tgc agc ggc gtc ctc atg cgg	1824
Ser Ala Gln Ala Gly Arg Leu Pro Ala Cys Ser Gly Val Leu Met Arg	
595 600 605	
cgg agg cca gcc cgc agg atc ctg agc cag gtc acc atg ctg gcg ttc	1872
Arg Arg Pro Ala Arg Arg Ile Leu Ser Gln Val Thr Met Leu Ala Phe	
610 615 620	
cag ggg gat gca ttg ctg gag cag atc agc gtc atc ggc ggg aac ctc	1920
Gln Gly Asp Ala Leu Leu Glu Gln Ile Ser Val Ile Gly Gly Asn Leu	
625 630 635 640	
acg ggc atc ttc atc cac cgg gtc acc ccg ggc tcg gcg gcg gac cag	1968
Thr Gly Ile Phe Ile His Arg Val Thr Pro Gly Ser Ala Ala Asp Gln	
645 650 655	
atg gcc ttg cgc ccg ggc acc cag att gtg atg gtt gat tac gaa gcc	2016
Met Ala Leu Arg Pro Gly Thr Gln Ile Val Met Val Asp Tyr Glu Ala	
660 665 670	
tca gag ccc ttg ttc aag gca gtc ctg gag gac acg acc ctg gag gag	2064
Ser Glu Pro Leu Phe Lys Ala Val Leu Glu Asp Thr Thr Leu Glu Glu	
675 680 685	
gcc gtg ggg ctt ctc agg agg gtg gac ggc ttc tgc tgc ctg tct gtg	2112
Ala Val Gly Leu Leu Arg Arg Val Asp Gly Phe Cys Cys Leu Ser Val	
690 695 700	
aag gtc aac acg gac ggt tat aag agg cta ctc cag gac ctg gag gcc	2160
Lys Val Asn Thr Asp Gly Tyr Lys Arg Leu Leu Gln Asp Leu Glu Ala	
705 710 715 720	
aaa gtg gcg acc tcg ggg gac tca ttc tac atc cgg gtc aac ctg gcc	2208

A1

T30290"STE260"

[illegible]

945	950								955						960				
tgc acc ctg cac agg atg gac atc ttc ccc atc gtc atc cac gtc tct Cys Thr Leu His Arg Met Asp Ile Phe Pro Ile Val Ile His Val Ser																			2928
965								970						975					
gtc aac gag aag atg gca aag aag ctc aag aag ggc cta cag cgg ttg Val Asn Glu Lys Met Ala Lys Lys Leu Lys Lys Gly Leu Gln Arg Leu																			2976
980								985						990					
ggc acc tca gag gag cag ctc ctg gag gct gcg agg cag gag gag gga Gly Thr Ser Glu Glu Gln Leu Leu Glu Ala Ala Arg Gln Glu Glu Gly																			3024
995								1000						1005					
gac ctg gac cgg gcg ccc tgt cta tac agc agc ctg gct cct gac ggc Asp Leu Asp Arg Ala Pro Cys Leu Tyr Ser Ser Leu Ala Pro Asp Gly																			3072
1010								1015						1020					
tgg agc gac ctg gac ggc ctg ctc agc tgt gtc cgc cag gcc atc gcc Trp Ser Asp Leu Asp Gly Leu Leu Ser Cys Val Arg Gln Ala Ile Ala																			3120
1025								1030						1035				1040	
gac gag cag aag aag gtg caa cgc cga cgt cat cca aga att aac cca Asp Glu Gln Lys Lys Val Gln Arg Arg Arg His Pro Arg Ile Asn Pro																			3168
1045								1050						1055					
agc cag agg acg ggc atc gcc acc cag caa cgc cag tgt cac cga aga Ser Gln Arg Thr Gly Ile Ala Thr Gln Gln Arg Gln Cys His Arg Arg																			3216
1060								1065						1070					
att aac cca agg cag agg atg ggc att gcc acc cag caa cgc cag tgt Ile Asn Pro Arg Gln Arg Met Gly Ile Ala Thr Gln Gln Arg Gln Cys																			3264
1075								1080						1085					
cac cga aga att aac cca agc cag agg acg ggc atc acc acc cag caa His Arg Arg Ile Asn Pro Ser Gln Arg Thr Gly Ile Thr Thr Gln Gln																			3312
1090								1095						1100					
tgc cag tgt cac cga aga att aac cca agc cag agg acg ggc atc gcc Cys Gln Cys His Arg Arg Ile Asn Pro Ser Gln Arg Thr Gln Arg Thr Gly Ile Ala																			3360
1105								1110						1115				1120	
atg cct tca tct tcg gac act ctc aaa aaa gat aag ctt ctg ccc aga Met Pro Ser Ser Ser Asp Thr Leu Lys Lys Asp Lys Leu Leu Pro Arg																			3408
1125								1130						1135					
aac acc aca Asn Thr Thr																			3417

```
<210> 5
<211> 1138
<212> PRT
<213> Homo sapiens
```

<400> 5
Gly Glu Leu Cys Arg Arg Asp Ser Ala Leu Thr Ala Leu Asp Glu Glu
1 5 10 15

Al

[illegible]

A1

[illegible]

Ser Gly Gly Arg Cys Trp Val Thr Arg His Ala Val Glu Ser Leu Met
 930 935 940
 Glu Lys Asn Thr His Ala Leu Leu Asp Val Gln Leu Asp Ser Val Cys
 945 950 955 960
 Thr Leu His Arg Met Asp Ile Phe Pro Ile Val Ile His Val Ser Val
 965 970 975
 Asn Glu Lys Met Ala Lys Lys Leu Lys Lys Gly Leu Gln Arg Leu Gly
 980 985 990
 Thr Ser Glu Glu Gln Leu Leu Glu Ala Ala Arg Gln Glu Gly Asp
 995 1000 1005
 Leu Asp Arg Ala Pro Cys Leu Tyr Ser Ser Leu Ala Pro Asp Gly Trp
 1010 1015 1020
 Ser Asp Leu Asp Gly Leu Leu Ser Cys Val Arg Gln Ala Ile Ala Asp
 1025 1030 1035 1040
 Glu Gln Lys Lys Val Gln Arg Arg Arg His Pro Arg Ile Asn Pro Ser
 1045 1050 1055
 Gln Arg Thr Gly Ile Ala Thr Gln Gln Arg Gln Cys His Arg Arg Ile
 1060 1065 1070
 Asn Pro Arg Gln Arg Met Gly Ile Ala Thr Gln Gln Arg Gln Cys His
 1075 1080 1085
 Arg Arg Ile Asn Pro Ser Gln Arg Thr Gly Ile Thr Thr Gln Gln Cys
 1090 1095 1100
 Gln Cys His Arg Arg Ile Asn Pro Ser Gln Arg Thr Gly Ile Ala Met
 1105 1110 1115 1120
 Pro Ser Ser Ser Asp Thr Leu Lys Lys Asp Lys Leu Leu Pro Arg Asn
 1125 1130 1135
 Thr Thr

<210> 6
 <211> 90
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<400> 6
 Ala Glu Asp Asp Arg Arg Leu Leu Arg Lys Asn Arg Leu Glu Leu Leu
 1 5 10 15
 Gly Glu Leu Thr Leu Ser Gly Leu Leu Asp His Leu Leu Glu Lys Asn
 20 25 30
 Val Leu Thr Glu Glu Glu Glu Lys Ile Lys Ala Lys Asn Thr Thr
 35 40 45
 Arg Arg Asp Lys Ala Arg Glu Leu Ile Asp Ser Val Gln Lys Lys Gly
 50 55 60
 Asn Gln Ala Phe Gly Ile Phe Leu Gln Ala Leu Arg Glu Thr Asp Gly
 65 70 75 80
 Glu Leu Leu Ala Asp Leu Leu Leu Asp Glu
 85 90

<210> 7
 <211> 83
 <212> PRT
 <213> Artificial Sequence

<220>

007674E 063004

A1

<223> consensus sequence

<400> 7

Glu Ile Thr Leu Glu Lys Glu Val Lys Arg Gly Gly Leu Gly Phe Ser
 1 5 10 15
 Ile Lys Gly Gly Ser Asp Lys Gly Ile Val Val Ser Glu Val Leu Pro
 20 25 30
 Gly Ser Gly Ala Ala Glu Ala Gly Gly Arg Leu Lys Glu Gly Asp Val
 35 40 45
 Ile Leu Ser Val Asn Gly Gln Asp Val Glu Asn Met Ser His Glu Arg
 50 55 60
 Ala Val Leu Ala Ile Lys Gly Ser Gly Gly Glu Val Thr Leu Thr Val
 65 70 75 80
 Leu Arg Asp

<210> 8

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<400> 8

Glu Tyr Val Val Ala Leu Tyr Asp Tyr Glu Ala Gln Asn Glu Asp Glu
 1 5 10 15
 Leu Ser Phe Lys Lys Gly Asp Ile Ile Thr Val Leu Glu Lys Ser Asp
 20 25 30
 Asp Gly Trp Trp Glu Gly Glu Leu Asn Arg Thr Gly Lys Glu Gly Leu
 35 40 45
 Phe Pro Ser Asn Tyr Val Glu Glu Ile Glu
 50 55

<210> 9

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<400> 9

Thr Arg Pro Val Pro Arg Pro Gly Glu Val Asp Gly Lys Asp Tyr His
 1 5 10 15
 Phe Val Ser Ser Arg Glu Glu Met Glu Lys Asp Ile Ala Ala Asn Glu
 20 25 30
 Phe Leu Glu Tyr Gly Glu Phe Gln Gly Asn Tyr Tyr Gly Thr Ser Leu
 35 40 45
 Glu Thr Val Arg Gln Val Ala Lys Gln Gly Lys Ile Cys Ile Leu Asp
 50 55 60
 Val Glu Pro Gln Gly Val Lys Arg Leu Arg Thr Ala Glu Leu Ser Asn
 65 70 75 80
 Pro Ile Val Val Phe Ile Ala Pro Pro Ser Leu Gln Glu Leu Glu Lys
 85 90 95
 Arg Leu Glu Gly Arg Asn Lys Glu Ser Glu Glu Ser
 100 105

AI

FORGOTTEN SECRETS

```
<220>
<223> consensus sequence
```

Asp 1	Ser	Tyr	Gln	Lys 5	Ser	Ser	Gly	Asn 10	Ser	Ser	Leu	Trp	Glu	Ser 15	Asn
Tyr	Gln	Asn	Trp 20	Gln	Gln	Glu	Ala 25	Ala	Lys	Leu	Lys	Ala 30	Gln	Ile	Glu
Asn	Leu	Gln 35	Asn	Asn	Arg	Asn	Gln 40	Arg	His	Leu	Leu 45	Gly	Glu	Asp	Leu
Gly	Ser 50	Leu	Ser	Leu	Lys	Glu 55	Leu	Gln	Gln	Leu	Glu 60	Gln	Gln	Leu	Glu
Lys 65	Gly	Leu	Lys	His 70	Ile	Arg	Ser	Arg	Lys 75	Asn	Gln	Leu	Leu	Leu 80	Asp
Gln	Ile	Glu	Glu 85	Leu	Gln	Lys	Lys	Glu 90	Arg	Glu	Leu	Gln 95	Glu	Glu	Asn
Lys	Ala	Leu	Arg 100	Lys	Lys	Ile	Glu 105	Glu							

[illegible]